

Sma

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The protein Sma is an amyloidogenic protein that was found in a patient. It is related to a benign, $\kappa 4$ immunoglobulin light chain protein Len. Sma and Len differ in sequence at only eight positions. At present, the structural basis of amyloid formation is not well understood. Thus, the structure of Sma would be of interest as it expands the structural database of light chains that form amyloid.

Recombinant Sma prepared from *E. coli* was crystallized in two crystal forms. One was a hexagonal crystal form (similar to one of the crystal forms of Len) obtained from 25% PEG 4K, 0.1 M MES (pH = 5.6), and 0.05 M ZnAc with $a = b = 101.5 \text{ \AA}$ and $c = 69.8 \text{ \AA}$ in space group $P6_122$. However, this crystal form diffracted to only 2.9 \AA resolution at the Structural Biology Center's (SBC-CAT) beamline 19-ID as it contained a large amount of solvent ($V_M = 4.1$). The structure of Sma in this hexagonal form has been solved and refined to an R-factor of 24.5% and R-free of 29.4% ($8.0\text{--}2.9 \text{ \AA}$ data).

Sma was also crystallized in a second form from 18% PEG 8K, 0.1 M Tris (pH = 8.5), and 1 mM ZnAc. X-ray diffraction data to 2 \AA were collected at 19-ID using the second crystal form. These crystals belonged to space group $P2_12_1$ with unit cell dimensions of $a = 53.0 \text{ \AA}$, $b = 64.9 \text{ \AA}$, and $c = 147.5 \text{ \AA}$. This crystal form contained two independent V_L dimers per asymmetric unit ($V_M = 2.5$). A weak solution was obtained by molecular replacement using the model of Sma from the hexagonal crystal form (R-factor of 42.8% and R-free of 43.9% for $8.0\text{--}3.5 \text{ \AA}$ data). Further refinement of this model is in progress.

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